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PCT10

RAW SEQUENCE LISTING

DATE: 04/17/2002

PATENT APPLICATION: US/10/089,600

TIME: 12:12:03

Input Set : A:\Q69170 Sequence Listing.txt

Output Set: N:\CRF3\04172002\J089600.raw

ENTERED

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3 <110> APPLICANT: Teijin Limited
5 <120> TITLE OF INVENTION: A NOVEL POLYPEPTIDE AND GENE ENCODING THE SAME
7 <130> FILE REFERENCE: Q69170
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/089,600
C--> 9 <141> CURRENT FILING DATE: 2002-03-29
9 <150> PRIOR APPLICATION NUMBER: PCT/JP00/06804
10 <151> PRIOR FILING DATE: 2000-09-29
12 <150> PRIOR APPLICATION NUMBER: JP 11-275947
13 <151> PRIOR FILING DATE: 1999-09-29
15 <160> NUMBER OF SEQ ID NOS: 25
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1200
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (67)..(1020)
27 <223> OTHER INFORMATION:
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31 ctccacctca gcaggtgtct ctcagtcctc tcaaagcaag gaaagagtac tgtgtgctga      60
33 gagacc atg gca aag aat cct cca gag aat tgt gaa gac tgt cac att      108
34      Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile
35          1              5              10
37 cta aat gca gaa gct ttt aaa tcc aag aaa ata tgt aaa tca ctt aag      156
38 Leu Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys
39 15              20              25              30
41 att tgt gga ctg gtg ttt ggt atc ctg gcc cta act cta att gtc ctg      204
42 Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val Leu
43          35              40              45
45 ttt tgg ggg agc aag cac ttc tgg ccg gag gta ccc aaa aaa gcc tat      252
46 Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys Ala Tyr
47          50              55              60
49 gac atg gag cac act ttc tac agc aat gga gag aag aag aag att tac      300
50 Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys Lys Ile Tyr
51          65              70              75
53 atg gaa att gat cct gtg acc aga act gaa ata ttc aga agc gga aat      348
54 Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe Arg Ser Gly Asn
55          80              85              90
57 ggc act gat gaa aca ttg gaa gta cac gac ttt aaa aac gga tac act      396
58 Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe Lys Asn Gly Tyr Thr
59 95              100              105              110
61 ggc atc tac ttc gtg ggt ctt caa aaa tgt ttt atc aaa act cag att      444

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62 Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys Phe Ile Lys Thr Gln Ile
63      115      120      125
65 aaa gtg att cct gaa ttt tct gaa cca gaa gag gaa ata gat gag aat      492
66 Lys Val Ile Pro Glu Phe Ser Glu Pro Glu Glu Glu Ile Asp Glu Asn
67      130      135      140
69 gaa gaa att acc aca act ttc ttt gaa cag tca gtg att tgg gtc cca      540
70 Glu Glu Ile Thr Thr Thr Phe Phe Glu Gln Ser Val Ile Trp Val Pro
71      145      150      155
73 gca gaa aag cct att gaa aac cga gat ttt ctt aaa aat tcc aaa att      588
74 Ala Glu Lys Pro Ile Glu Asn Arg Asp Phe Leu Lys Asn Ser Lys Ile
75      160      165      170
77 ctg gag att tgt gat aac gtg acc atg tat tgg atc aat ccc act cta      636
78 Leu Glu Ile Cys Asp Asn Val Thr Met Tyr Trp Ile Asn Pro Thr Leu
79 175      180      185      190
81 ata tca gtt tct gag tta caa gac ttt gag gag gag gga gaa gat ctt      684
82 Ile Ser Val Ser Glu Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu
83      195      200      205
85 cac ttt cct gcc aac gaa aaa aaa ggg att gaa caa aat gaa cag tgg      732
86 His Phe Pro Ala Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp
87      210      215      220
89 gtg gtc cct caa gtg aaa gta gag aag acc cgt cac gcc aga caa gca      780
90 Val Val Pro Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala
91      225      230      235
93 agt gag gaa gaa ctt cca ata aat gac tat act gaa aat gga ata gaa      828
94 Ser Glu Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu
95      240      245      250
97 ttt gat ccc atg ctg gat gag aga ggt tat tgt tgt att tac tgc cgt      876
98 Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg
99 255      260      265      270
101 cga ggc aac cgc tat tgc cgc cgc gtc tgt gaa cct tta cta ggc tac      924
102 Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly Tyr
103      275      280      285
105 tac cca tat cca tac tgc tac caa gga gga cga gtc atc tgt cgt gtc      972
106 Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg Val
107      290      295      300
109 atc atg cct tgt aac tgg tgg gtg gcc cgc atg ctg ggg agg gtc taa      1020
110 Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val
111      305      310      315
113 taggaggttt gagctcaaat gcttaaactg ctggcaacat ataataaatg catgctattc      1080
115 aatgaatttc tgcctatgag gcatctggcc cctggtagcc agctctccag aattacttgt      1140
117 aggtaattcc tctcttcattg ttctaataaaa cttctacatt atcaccaaaa aaaaaaaaaa      1200
120 <210> SEQ ID NO: 2
121 <211> LENGTH: 317
122 <212> TYPE: PRT
123 <213> ORGANISM: Homo sapiens
125 <400> SEQUENCE: 2
127 Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu Asn
128 1      5      10      15
131 Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys Ile Cys

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132          20          25          30
135 Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val Leu Phe Trp
136          35          40          45
139 Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys Ala Tyr Asp Met
140          50          55          60
143 Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys Lys Ile Tyr Met Glu
144 65          70          75          80
147 Ile Asp Pro Val Thr Arg Thr Glu Ile Phe Arg Ser Gly Asn Gly Thr
148          85          90          95
151 Asp Glu Thr Leu Glu Val His Asp Phe Lys Asn Gly Tyr Thr Gly Ile
152          100          105          110
155 Tyr Phe Val Gly Leu Gln Lys Cys Phe Ile Lys Thr Gln Ile Lys Val
156          115          120          125
159 Ile Pro Glu Phe Ser Glu Pro Glu Glu Glu Ile Asp Glu Asn Glu Glu
160          130          135          140
163 Ile Thr Thr Thr Phe Phe Glu Gln Ser Val Ile Trp Val Pro Ala Glu
164 145          150          155          160
167 Lys Pro Ile Glu Asn Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu
168          165          170          175
171 Ile Cys Asp Asn Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser
172          180          185          190
175 Val Ser Glu Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe
176          195          200          205
179 Pro Ala Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val
180          210          215          220
183 Pro Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu
184 225          230          235          240
187 Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe Asp
188          245          250          255
191 Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg Arg Gly
192          260          265          270
195 Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly Tyr Tyr Pro
196          275          280          285
199 Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg Val Ile Met
200          290          295          300
203 Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val
204 305          310          315
207 <210> SEQ ID NO: 3
208 <211> LENGTH: 1180
209 <212> TYPE: DNA
210 <213> ORGANISM: Mus musculus
212 <220> FEATURE:
213 <221> NAME/KEY: CDS
214 <222> LOCATION: (59)..(1012)
215 <223> OTHER INFORMATION:
218 <400> SEQUENCE: 3
219 agcagtagtc ctctcagtc tctcaaagca gggaaagagc accgtgtgct gggagacc      58
221 atg gca aag aat cct cca gag aac tgt gag ggc tgt cac att cta aat      106
222 Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Gly Cys His Ile Leu Asn

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223	1	5	10	15	
225	gca gaa gct ctg aaa tct aag aag ata tgt aaa tca ctg aag att tgt	154			
226	Ala Glu Ala Leu Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys Ile Cys				
227	20 25 30				
229	gga cta gtg ttt ggt atc ctg gcc tta act cta att gtc ctg ttt tgg	202			
230	Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val Leu Phe Trp				
231	35 40 45				
233	ggg agc aaa cac ttc tgg ccc gag gta tcc aag aaa acc tat gac atg	250			
234	Gly Ser Lys His Phe Trp Pro Glu Val Ser Lys Lys Thr Tyr Asp Met				
235	50 55 60				
237	gag cac act ttc tac agc aac ggc gag aag aag aag att tac atg gaa	298			
238	Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys Lys Ile Tyr Met Glu				
239	65 70 75 80				
241	att gat ccc ata acc aga aca gaa ata ttc aga agt gga aat ggc act	346			
242	Ile Asp Pro Ile Thr Arg Thr Glu Ile Phe Arg Ser Gly Asn Gly Thr				
243	85 90 95				
245	gat gaa aca ttg gaa gtc cat gac ttt aaa aat gga tac act ggc atc	394			
246	Asp Glu Thr Leu Glu Val His Asp Phe Lys Asn Gly Tyr Thr Gly Ile				
247	100 105 110				
249	tac ttt gta ggt ctt caa aaa tgc ttt att aaa act caa atc aaa gtg	442			
250	Tyr Phe Val Gly Leu Gln Lys Cys Phe Ile Lys Thr Gln Ile Lys Val				
251	115 120 125				
253	att cct gaa ttt tct gaa cca gag gaa gaa ata gat gag aat gaa gaa	490			
254	Ile Pro Glu Phe Ser Glu Pro Glu Glu Glu Ile Asp Glu Asn Glu Glu				
255	130 135 140				
257	att act aca act ttc ttt gaa cag tca gtg att tgg gtt ccc gca gaa	538			
258	Ile Thr Thr Thr Phe Phe Glu Gln Ser Val Ile Trp Val Pro Ala Glu				
259	145 150 155 160				
261	aag cct att gaa aac aga gac ttc ctg aaa aat tct aaa att ctg gag	586			
262	Lys Pro Ile Glu Asn Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu				
263	165 170 175				
265	att tgc gat aat gtg acc atg tac tgg atc aat ccc act cta ata gca	634			
266	Ile Cys Asp Asn Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ala				
267	180 185 190				
269	gtt tca gaa tta cag gac ttt gag gag gac ggt gaa gat ctt cac ttt	682			
270	Val Ser Glu Leu Gln Asp Phe Glu Glu Asp Gly Glu Asp Leu His Phe				
271	195 200 205				
273	cct acc agt gaa aaa aag ggg att gac cag aat gag caa tgg gtg gtc	730			
274	Pro Thr Ser Glu Lys Lys Gly Ile Asp Gln Asn Glu Gln Trp Val Val				
275	210 215 220				
277	ccg caa gtg aag gtg gag aag acc cgc cac acc aga caa gca agc gag	778			
278	Pro Gln Val Lys Val Glu Lys Thr Arg His Thr Arg Gln Ala Ser Glu				
279	225 230 235 240				
281	gaa gac ctt cct ata aat gac tat act gaa aat gga att gaa ttt gac	826			
282	Glu Asp Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe Asp				
283	245 250 255				
285	cca atg ctg gat gag aga ggt tac tgt tgt att tac tgt cgt cga ggc	874			
286	Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg Arg Gly				
287	260 265 270				

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PATENT APPLICATION: US/10/089,600

DATE: 04/17/2002

TIME: 12:12:03

Input Set : A:\Q69170 Sequence Listing.txt

Output Set: N:\CRF3\04172002\J089600.raw

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289 aac cgt tac tgc cgc cgt gtc tgt gaa cct tta cta ggc tac tac cca      922
290 Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly Tyr Tyr Pro
291      275      280      285
293 tac ccc tac tgc tac caa gga ggt cga gtc atc tgt cgt gtc atc atg      970
294 Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg Val Ile Met
295      290      295      300
297 cct tgc aac tgg tgg gtg gcc cgc atg ctt ggg aga gtc taa
298 Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val      1012
299 305      310      315
301 taggaagatt gagttcaaac gcttaacctt ctgtaggcca atatataatt aatgcatgct      1072
303 actccatgaa tttctgccta tgaggcattt gcctccaagt agcctatcct tcagaattac      1132
305 ttgtaggata ttctctctct catgttctaa taaacttcta catcatca      1180
308 <210> SEQ ID NO: 4
309 <211> LENGTH: 317
310 <212> TYPE: PRT
311 <213> ORGANISM: Mus musculus
313 <400> SEQUENCE: 4
315 Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Gly Cys His Ile Leu Asn
316 1      5      10      15
319 Ala Glu Ala Leu Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys Ile Cys
320      20      25      30
323 Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val Leu Phe Trp
324      35      40      45
327 Gly Ser Lys His Phe Trp Pro Glu Val Ser Lys Lys Thr Tyr Asp Met
328      50      55      60
331 Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys Lys Ile Tyr Met Glu
332 65      70      75      80
335 Ile Asp Pro Ile Thr Arg Thr Glu Ile Phe Arg Ser Gly Asn Gly Thr
336      85      90      95
339 Asp Glu Thr Leu Glu Val His Asp Phe Lys Asn Gly Tyr Thr Gly Ile
340      100      105      110
343 Tyr Phe Val Gly Leu Gln Lys Cys Phe Ile Lys Thr Gln Ile Lys Val
344      115      120      125
347 Ile Pro Glu Phe Ser Glu Pro Glu Glu Glu Ile Asp Glu Asn Glu Glu
348      130      135      140
351 Ile Thr Thr Thr Phe Phe Glu Gln Ser Val Ile Trp Val Pro Ala Glu
352 145      150      155      160
355 Lys Pro Ile Glu Asn Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu
356      165      170      175
359 Ile Cys Asp Asn Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ala
360      180      185      190
363 Val Ser Glu Leu Gln Asp Phe Glu Glu Asp Gly Glu Asp Leu His Phe
364      195      200      205
367 Pro Thr Ser Glu Lys Lys Gly Ile Asp Gln Asn Glu Gln Trp Val Val
368      210      215      220
371 Pro Gln Val Lys Val Glu Lys Thr Arg His Thr Arg Gln Ala Ser Glu
372 225      230      235      240
375 Glu Asp Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe Asp
376      245      250      255

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/089,600

DATE: 04/17/2002

TIME: 12:12:04

Input Set : A:\Q69170 Sequence Listing.txt

Output Set: N:\CRF3\04172002\J089600.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date